SEQUENCE LISTING

<110> Human Genome Sciences, Inc.

<120> Albumin Fusion Proteins

<130> PF547PCT

<140> 09/832,929
<141> 2001-04-12

<150> 60/229,358
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<151> 2000-12-21

<150> 60/199,384
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<170> PatentIn Ver. 2.1

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Ile Ser Ala Asp Ala His Lys Ser
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fragments with non-cohesive ends.

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ac   62

<210> 16
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fragments with non-cohesive ends.

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gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag      96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
                 20                  25                  30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa     144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
             35                  40                  45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa     192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
         50                  55                  60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt     240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65                  70                  75                  80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct     288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                 85                  90                  95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc     336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
                100                 105                 110

ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat     384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
            115                 120                 125

gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga     432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
        130                 135                 140

aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg     480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc     528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175
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6

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tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg    576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa    624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
            195                 200                 205

aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc    672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa    720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac    768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc    816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac    864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
            275                 280                 285

tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca    912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct    960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga   1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca   1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa   1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
            355                 360                 365

tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct   1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380
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7

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cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag   1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc   1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa   1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
                420                 425                 430

gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt   1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
                435                 440                 445

gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat   1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
        450                 455                 460

gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc   1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca   1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat   1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
                500                 505                 510

ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca   1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
            515                 520                 525

ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg   1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
            530                 535                 540

aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag   1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt   1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag 1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu
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<210> 18
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<213> Homo Sapiens

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Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
            35   40   45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
        50   55   60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65   70   75   80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85   90   95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100   105   110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115   120   125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130   135   140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145   150   155   160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165   170   175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180   185   190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
            195   200   205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210   215   220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225   230   235   240

9

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245   250   255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
                260   265   270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
                275   280   285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290   295   300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305   310   315   320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325   330   335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
                340   345   350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
                355   360   365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370   375   380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385   390   395   400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405   410   415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
                420   425   430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
                435   440   445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450   455   460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465   470   475   480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485   490   495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
                500   505   510

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Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
         515                 520             525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535             540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
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Ala Ala Ser Gln Ala Ala Leu Gly Leu
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<223> Synthetic oligonucleotide used to alter restriction
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<400> 23
aagctgcctt aggcttataa taaggcgcgc cggccggccg tttaaactaa gcttaattct 60


<210> 24
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sites in pPPC0007

<400> 24
agaattaagc ttagtttaaa cggccggccg gcgcgcctta ttataagcct aaggcagctt 60


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<223> forward primer useful for generation of albumin
fusion protein in which the albumin  moiety is N-terminal
of the Therapeutic Protein

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protein in which the albumin moiety is c-terminal of the
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (50)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (51)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<400> 28
ctttaaatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnn nn          52


<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> signal peptide of natural human serum albumin protein
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<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
  1   5   10   15

Tyr Ser Arg Ser Leu Asp Lys Arg
                20

<210> 30
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of PC4:HSA
albumin fusion VECTOR

<220>
<221> misc_feature
<222> (5)..(10)
<223> BamHI retsriction site

<220>
<221> misc_feature
<222> (11)..(16)
<223> Hind III retsriction site

<220>
<221> misc_feature
<222> (17)..(27)
<223> Kozak sequence

<220>
<221> misc_feature
<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

<220>
<221> misc_feature
<222> (75)..(81)
<223> XhoI restriction site

<220>
<221> misc_feature
<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcagggatcc aagcttccgc caccatgaag tgggtaacct ttatttccct tcttttctc 60

tttagctcgg cttactcgag gggtgtgttt cgtcgagatg cacacaagag tgag   114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
<221> misc_feature
<222> (6)..(11)
<223> Asp718 restriction site

<220>
<221> misc_feature
<222> (12)..(17)
<223> EcoRI restriction site

<220>
<221> misc_feature
<222> (15)..(17)
<223> reverse complement of stop codon

<220>
<221> misc_feature
<222> (18)..(25)
<223> AscI restriction site

<220>
<221> misc_feature
<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtac cgaattcggc gcgccttata agcctaaggc agc   43

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc feature
<222> (29)

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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (34)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (35)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (37)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c
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<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<400> 32
ccgccgctcg aggggtgtgt ttcgtcgann nnnnnnnnn nnnnn   46

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

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<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (48)
<223> n equals a,t,g, or c

<220>
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<221> misc feature
<222> (49)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (50)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (51)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (53)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<400> 33
agtcccatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnnn nnnnn   55

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
 1   5   10   15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
 1   5   10   15

Trp Ala Pro Ala Arg Gly
                20

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 36
caggtgcagc tggtgcagtc tgg   23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 37
caggtcaact taagggagtc tgg   23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

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<400> 38
gaggtgcagc tggtggagtc tgg                                    23


<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 39
caggtgcagc tgcaggagtc ggg                                    23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 40
gaggtgcagc tgttgcagtc tgc                                    23


<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 41
caggtacagc tgcagcagtc agg                                    23

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
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<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 42
tgaggagacg gtgaccaggg tgcc   24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 43
tgaagagacg gtgaccattg tccc   24

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 44
tgaggagacg gtgaccaggg ttcc   24

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 45
tgaggagacg gtgaccgtgg tccc   24

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind

<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 46
gacatccaga tgacccagtc tcc   23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 47
gatgttgtga tgactcagtc tcc   23

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 48
gatattgtga tgactcagtc tcc   23

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 49
gaaattgtgt tgacgcagtc tcc   23

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind

29

<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 50
gacatcgtga tgacccagtc tcc   23

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 51
gaaacgacac tcacgcagtc tcc   23

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 52
gaaattgtgc tgactcagtc tcc   23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 53
cagtctgtgt tgacgcagcc gcc   23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind

<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 54
cagtctgccc tgactcagcc tgc   23

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 55
tcctatgtgc tgactcagcc acc   23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 56
tcttctgagc tgactcagga ccc   23

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 57
cacgttatac tgactcaacc gcc   23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind

<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 58
caggctgtgc tcactcagcc gtc   23

<210> 59
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 59
aattttatgc tgactcagcc cca   23

<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 60
acgtttgatt tccaccttgg tccc   24

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 61
acgtttgatc tccagcttgg tccc   24

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind

<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 62
acgtttgata tccactttgg tccc   24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 63
acgtttgatc tccaccttgg tccc   24

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 64
acgtttaatc tccagtcgtg tccc   24

<210> 65
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 65
cagtctgtgt tgacgcagcc gcc   23

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind

<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 66
cagtctgccc tgactcagcc tgc   23

<210> 67
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 67
tcctatgtgc tgactcagcc acc   23

<210> 68
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 68
tcttctgagc tgactcagga ccc   23

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 69
cacgttatac tgactcaacc gcc   23

<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind

<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 70
caggctgtgc tcactcagcc gtc   23

<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 71
aattttatgc tgactcagcc cca   23

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221>turn   `
<223>Linker peptide that may be used to join VH
and VL domains in an scFv.

<400> 72
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
  1   5   10   15

<210> 73
<211> 733
<212> DNA
<213> Homo sapiens

<400> 73
gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg
60

aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga
120

tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg
180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg
240

aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact
300

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg
360

agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc
420

catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct
480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga
540

ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg
600

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc
660

acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc
720

gactctagag gat
733

<210> 74
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<221> misc_structure
<223> membrane proximal motif of class 1 cytokine receptors

<220>
<221> misc_feature
<222> (3)
<223> Xaa equals any

<400> 74
Trp Ser Xaa Trp Ser
  1   5

<210> 75
<211> 86
<212> DNA
<213> Artificial Sequence

36

<220>
<221> primer_bind
<223> forward primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 75
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc
60

cccgaaatat ctgccatctc aattag
86

<210> 76
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 76
gcggcaagct ttttgcaaag cctaggc
27

<210> 77
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Synthetic GAS-SV40 promoter sequence

<400> 77
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg
60

aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc
120

gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat
180

ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt
240

ttttggaggc ctaggctttt gcaaaaagct t
271

<210> 78
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 78
gcgctcgagg gatgacagcg atagaacccc gg
32

<210> 79
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 79
gcgaagcttc gcgactcccc ggatccgcct c
31

<210> 80
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_binding
<223> NF-KB binding site

<400> 80
ggggactttc cc
12

<210> 81
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of a vector containing the NF-KB promoter element

<400> 81
gcggcctcga ggggactttc ccggggactt ccggggact ttccgggact ttccatcctg
60

ccatctcaat tag
73

<210> 82
<211> 256
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Synthetic NF-KB/SV40 promoter

<400> 82
ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct
60

caattagtca gcaaccatag tcccgcccct aactccgccc atcccgcccc taactccgcc
120

cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga
180

ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg
240

cttttgcaaa aagctt
256